



SEQUENCE LISTING

<110> WUCHERPFENNIG, Kai W
STROMINGER, Jack L

<120> MONOVALENT, MULTIVALENT AND MULTIMERIC MHC BINDING DOMAIN FUSION PROTEINS AND CONJUGATES, AND USES THEREFOR

<130> HAR-005

<140> 09/248,964
<141> 1999-02-12

<150> PCT/US97/14503
<151> 1997-08-15

<150> 60/075,351
<151> 1998-02-19

<150> 60/024,077
<151> 1996-08-15

<160> 14

<170> PatentIn Ver. 2.0

<210> 1
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-Fos fusion

<220>
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<222> (1)..(735)

<220>
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<222> (1)..(21)
<223> 3' end of secretory signal

<220>
<221> misc_structure
<222> (22)..(594)
<223> DRA*0101 extracellular domain

<220>
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<222> (595)..(615)
<223> Linker sequence

<220>
<221> misc_feature
<222> (616)..(735)
<223> Fos leucine zipper domain
<400> 1

gta tct ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag 48

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TECH CENTER 1600/2900

Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln
1 5 10 15

gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac 96
Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
20 25 30

ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg
144
Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
35 40 45

gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa
192
Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
50 55 60

ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg
240
Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
65 70 75 80

aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta
288
Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
85 90 95

act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc
336
Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
100 105 110

atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg
384
Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
115 120 125

ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc
432
Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
130 135 140

ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc
480
Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
145 150 155 160

ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc
528
Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
165 170 175

ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct
576
Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
180 185 190

ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat
624

Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu Thr Asp
195 200 205

aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg
672

Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu
210 215 220

cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc
720

Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
225 230 235 240

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Ile Leu Ala Ala His
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<210> 2

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Fos fusion

<220>

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<222> (1)..(7)

<223> 3' end of secretory signal

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<221> misc_structure

<222> (8)..(198)

<223> DRA*0101 extracellular domain

<220>

<221> misc_feature

<222> (199)..(205)

<223> Linker sequence

<220>

<221> misc_feature

<222> (206)..(245)

<223> Fos leucine zipper domain

<400> 2

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20 25 30

Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
35 40 45

Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
50 55 60

Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
65 70 75 80

Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
85 90 95

Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
100 105 110

Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
115 120 125

Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
130 135 140

Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
145 150 155 160

Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
165 170 175

Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
180 185 190

Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu Thr Asp
195 200 205

Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu
210 215 220

Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
225 230 235 240

Ile Leu Ala Ala His
245

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Jun fusion

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<222> (1)...(756)

<220>

<221> misc_feature

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<221> misc_feature

<222> (22)...(615)

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 <222> (616)..(636)
 <223> Linker sequence

<220>
 <221> misc_feature
 <222> (637)..(756)
 <223> Jun leucine zipper domain

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1									10						15	

cag cct aag agg gag tgt cat ttc ttc aat ggg acg gag cg^g gtg cg^g 96
 Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
 20 25 30

ttc ctg gac aga tac ttc tat aac cag gag gag tcc gtg cgc ttc gac
 144
 Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
 35 40 45

agc gac gtg ggg gag ttc cg^g gc^g gtg acg gag ctg ggg cg^g cct gac
 192
 Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
 50 55 60

gct gag tac tgg aac agc cag aag gac atc ctg gag cag gc^g cg^g gcc
 240
 Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
 65 70 75 80

gc^g gtg gac acc tac tgc aga cac aac tac ggg gtt gtg gag agc ttc
 288
 Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
 85 90 95

aca gtg cag cg^g cga gtc caa cct aag gtg act gta tat cct tca aag
 336
 Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
 100 105 110

acc cag ccc ctg cag cac cac aac ctc ctg gtc tgc tct gtg agt ggt
 384
 Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
 115 120 125

ttc tat cca ggc agc att gaa gtc agg tgg ttc ctg aac ggc cag gaa
 432
 Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
 130 135 140

gag aag gct ggg atg gtg tcc aca ggc ctg atc cag aat gga gac tgg
 480
 Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
 145 150 155 160

acc ttc cag acc ctg gtg atg ctg gaa aca gtt cct cga agt gga gag
528

Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
165 170 175

gtt tac acc tgc caa gtg gag cac cca agc gtg aca agc cct ctc aca
576

Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
180 185 190

gtg gaa tgg aga gca cg^g tct gaa tct gca cag agc aag gtc gac gga
624

Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
195 200 205

ggt ggc ggc ggt cgc atc gcc cg^g ctc gag gaa aaa gtg aaa acc ttg
672

Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
210 215 220

aaa gct cag aac tcg gag ctc gc^g tcc acg gcc aac atg ctc agg gaa
720

Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
225 230 235 240

cag gtg gca cag ctt aaa cag aaa gtc atg aac cat tgagaattct atgac
771

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245 250

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Jun fusion

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<223> 3' end of secretory signal

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<221> misc_feature

<222> (8)..(205)

<223> DRB1*1501 extracellular domain

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<221> misc_feature

<222> (206)..(212)

<223> Linker sequence

<220>

<221> misc_feature

<222> (213)..(252)

<223> Jun leucine zipper domain

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20 25 30
Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
35 40 45
Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
50 55 60
Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
65 70 75 80
Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
85 90 95
Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
100 105 110
Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
115 120 125
Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
130 135 140
Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
145 150 155 160
Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
165 170 175
Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
180 185 190
Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
195 200 205
Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
210 215 220
Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
225 230 235 240
Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
245 250

<210> 5
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

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<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 6
gtcatagaat tctcaatggg cggccaggat gaactccag 39

<210> 7
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 7
gtatctctcg agaaaagaga gggggacacc cgaccacgtt tc 42

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 8
gtcatagaat tctcaatggt tcgtgacttt ctgtttaag 39

<210> 9
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic, biotin ligase recognition sequence

<400> 9
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<210> 10
<211> 16

<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic,
linker sequence

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<210> 11
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<212> DNA
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<220>
<223> Description of Artificial Sequence: DR2-IgG fusion

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<222> (589)..(609)
<223> Linker

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<222> (610)..(729)
<223> Fos leucine zipper domain

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<221> misc_feature
<222> (730)..(1437)
<223> IgG domain

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1 5 10 15

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Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
20 25 30

ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg gtc tgg
144
Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
35 40 45

cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa ggt gca
192
Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
50 55 60

ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg aca aag
240
Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
65 70 75 80

cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta act gtg
288
Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
85 90 95

ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc atc tgt
336
Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
100 105 110

ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg ctt cga
384
Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg
115 120 125

aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc ctg ccc
432
Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro
130 135 140

agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc ctg ccc
480
Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro
145 150 155 160

tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc ttg gat
528
Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp
165 170 175

gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct ctc cca
576
Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro
180 185 190

gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat aca ctc
624
Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu Thr Asp Thr Leu
195 200 205

caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg cag acc
672
Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr

210 215 220

gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc atc ctg
720 Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu
225 230 235 240

gcc gcc cat gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt
768 Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
245 250 255

cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc
816 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
260 265 270

ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc
864 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
275 280 285

ccc ata gtc aca tgt gtg gtg gat gtg agc gag gat gac cca gat
912 Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
290 295 300

gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag
960 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
305 310 315 320

aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt
1008 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
325 330 335

gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa
1056 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
340 345 350

tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc
1104 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
355 360 365

tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct
1152 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
370 375 380

cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg
1200 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
385 390 395 400

gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac
1248
Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
405 410 415

ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct
1296
Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
420 425 430

gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac
1344
Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
435 440 445

tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg
1392
Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
450 455 460

cac aat cac cac acg act aag agc ttc tcc cg^g act ccg ggt aaa
1437
His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
465 470 475

tgagaattc
1446

<210> 12
<211> 479
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<220>
<223> Description of Artificial Sequence: DR2-IgG fusion

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<222> (6)..(196)
<223> DRA*0101 extracellular domain

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<222> (197)..(203)
<223> Linker

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<222> (204)..(243)
<223> Fos leucine zipper domain

<220>
<221> misc_feature

<222> (244)..(479)
<223> IgG domain

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Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
20 25 30

Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
35 40 45

Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
50 55 60

Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
65 70 75 80

Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
85 90 95

Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
100 105 110

Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg
115 120 125

Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro
130 135 140

Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro
145 150 155 160

Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp
165 170 175

Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro
180 185 190

Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu Thr Asp Thr Leu
195 200 205

Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr
210 215 220

Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu
225 230 235 240

Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
245 250 255

Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
260 265 270

Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser

275 280 285

Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
290 295 300

Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
305 310 315 320

Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
325 330 335

Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
340 345 350

Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
355 360 365

Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
370 375 380

Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
385 390 395 400

Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
405 410 415

Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
420 425 430

Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
435 440 445

Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
450 455 460

His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
465 470 475

<210> 13
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-IgM fusion

<220>
<221> CDS
<222> (1)..(1836)

<220>
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<222> (1)..(75)
<223> 3' end of secretory signal

<220>
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<222> (76)..(648)

<223> DRA*0101 extracellular domain
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 <222> (670)..(789)
 <223> Fos leucine zipper domain
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 <221> misc_feature
 <222> (790)..(1836)
 <223> IgG domain
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 Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
 1 5 10 15
 ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc 96
 Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
 20 25 30
 atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg
 144
 Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45
 ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag
 192
 Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60
 gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag 240
 288
 Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65 70 75 80
 gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa
 Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
 85 90 95
 atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca 336
 Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110
 gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac 384
 Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125
 gtc ctc atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc 432

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
130 135 140

acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca
480

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145 150 155 160

gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc
528

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
165 170 175

ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac
576

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
180 185 190

tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca
624

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
195 200 205

agc cct ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta
672

Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu
210 215 220

act gat aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct
720

Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
225 230 235 240

gcg ttg cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg
768

Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
245 250 255

gag ttc atc ctg gcc gcc cac gtc gca gaa atg aac ccc aat gta aat
816

Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn
260 265 270

gtg ttc gtc cca cca cgg gat ggc ttc tct ggc cct gca cca cgc aag
864

Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys
275 280 285

tct aaa ctc atc tgc gag gcc acg aac ttc act cca aaa ccg atc aca
912

Ser Lys Leu Ile Cys Glu Ala Thr Asn Phe Thr Pro Lys Pro Ile Thr
290 295 300

gta tcc tgg cta aag gat ggg aag ctc gtg gaa tct ggc ttc acc aca
960

Val Ser Trp Leu Lys Asp Gly Lys Leu Val Glu Ser Gly Phe Thr Thr
305 310 315 320

gat ccg gtg acc atc gag aac aaa gga tcc aca ccc caa acc tac aag
1008
Asp Pro Val Thr Ile Glu Asn Lys Gly Ser Thr Pro Gln Thr Tyr Lys
325 330 335

gtc ata agc aca ctt acc atc tct gaa atc gac tgg ctg aac ctg aat
1056
Val Ile Ser Thr Leu Thr Ile Ser Glu Ile Asp Trp Leu Asn Leu Asn
340 345 350

gtg tac acc tgc cgt gtg gat cac agg ggt ctc acc ttc ttg aag aac
1104
Val Tyr Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Leu Lys Asn
355 360 365

gtg tcc tcc aca tgt gct gcc agt ccc tcc aca gat atc ctt aat ttt
1152
Val Ser Ser Thr Cys Ala Ala Ser Pro Ser Thr Asp Ile Leu Asn Phe
370 375 380

act att cct cct tcc ttt gcc gac atc ttc ctt agc aag tcc gct aac
1200
Thr Ile Pro Pro Ser Phe Ala Asp Ile Phe Leu Ser Lys Ser Ala Asn
385 390 395 400

ctg acc tgt ctg gtc tca aac ctg gca acc tat gaa acc ctg agt atc
1248
Leu Thr Cys Leu Val Ser Asn Leu Ala Thr Tyr Glu Thr Leu Ser Ile
405 410 415

tcc tgg gct tct caa agt ggt gaa cca ctg gaa acc aaa att aaa atc
1296
Ser Trp Ala Ser Gln Ser Gly Glu Pro Leu Glu Thr Lys Ile Lys Ile
420 425 430

atg gaa agc cat ccc aat ggc acc ttc agt gct aag ggt gtg gct agt
1344
Met Glu Ser His Pro Asn Gly Thr Phe Ser Ala Lys Gly Val Ala Ser
435 440 445

gtt tgt gtg gaa gac tgg aat aac agg aag gaa ttt gtg tgt act gtg
1392
Val Cys Val Glu Asp Trp Asn Asn Arg Lys Glu Phe Val Cys Thr Val
450 455 460

act cac agg gat ctg cct tca cca cag aag aaa ttc atc tca aaa ccc
1440
Thr His Arg Asp Leu Pro Ser Pro Gln Lys Lys Phe Ile Ser Lys Pro
465 470 475 480

aat gag gtg cac aaa cat cca cct gct gtg tac ctg ctg cca cca gct
1488
Asn Glu Val His Lys His Pro Pro Ala Val Tyr Leu Leu Pro Pro Ala
485 490 495

cgt gaa caa ctg aac ctg agg gag tca gcc aca gtc acc tgc ctg gtg
1536
Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Val Thr Cys Leu Val
500 505 510

aag ggc ttc tct cct gca gac atc tct gtg caa tgg aag cag agg ggc
1584
Lys Gly Phe Ser Pro Ala Asp Ile Ser Val Gln Trp Lys Gln Arg Gly

515 520 525
cag ctc tta ccc cag gag aag tat gtg acc agt gcc ccg atg cca gag
1632
Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu
530 535 540

cct ggg gcc cca ggc ttc tac ttt acc cac agc atc ctg act gtg aca
1680
Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr
545 550 555 560

gag gag gaa tgg aac tcc gga gag acc tat acc tgt gtt gta ggc cac
1728
Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His
565 570 575

gag gcc ctg cca cac ctg gtg acc gag agg acc gtg gac aag tcc act
1776
Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr
580 585 590

ggt aaa ccc aca ctg tac aat gtc tcc ctg atc atg tct gac aca ggc
1824
Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
595 600 605

ggc acc tgc tat tgaagatctg tcgac
1851
Gly Thr Cys Tyr
610

<210> 14
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Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
      20          25          30

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
      35          40          45

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
      50          55          60

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
      65          70          75          80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
      85          90          95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
      100         105         110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
      115         120         125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
      130         135         140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
      145         150         155         160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
      165         170         175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
      180         185         190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
      195         200         205

Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu
      210         215         220

Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
      225         230         235         240

Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu

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245	250	255
Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn 260	265	270
Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys 275	280	285
Ser Lys Leu Ile Cys Glu Ala Thr Asn Phe Thr Pro Lys Pro Ile Thr 290	295	300
Val Ser Trp Leu Lys Asp Gly Lys Leu Val Glu Ser Gly Phe Thr Thr 305	310	315
Asp Pro Val Thr Ile Glu Asn Lys Gly Ser Thr Pro Gln Thr Tyr Lys 325	330	335
Val Ile Ser Thr Leu Thr Ile Ser Glu Ile Asp Trp Leu Asn Leu Asn 340	345	350
Val Tyr Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Leu Lys Asn 355	360	365
Val Ser Ser Thr Cys Ala Ala Ser Pro Ser Thr Asp Ile Leu Asn Phe 370	375	380
Thr Ile Pro Pro Ser Phe Ala Asp Ile Phe Leu Ser Lys Ser Ala Asn 385	390	395
Leu Thr Cys Leu Val Ser Asn Leu Ala Thr Tyr Glu Thr Leu Ser Ile 405	410	415
Ser Trp Ala Ser Gln Ser Gly Glu Pro Leu Glu Thr Lys Ile Lys Ile 420	425	430
Met Glu Ser His Pro Asn Gly Thr Phe Ser Ala Lys Gly Val Ala Ser 435	440	445
Val Cys Val Glu Asp Trp Asn Asn Arg Lys Glu Phe Val Cys Thr Val 450	455	460
Thr His Arg Asp Leu Pro Ser Pro Gln Lys Lys Phe Ile Ser Lys Pro 465	470	475
Asn Glu Val His Lys His Pro Pro Ala Val Tyr Leu Leu Pro Pro Ala 485	490	495
Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Val Thr Cys Leu Val 500	505	510
Lys Gly Phe Ser Pro Ala Asp Ile Ser Val Gln Trp Lys Gln Arg Gly 515	520	525
Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu 530	535	540
Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr 545	550	555
560		

Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His
565 570 575

Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr
580 585 590

Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
595 600 605

Gly Thr Cys Tyr
610